

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Seed, Brian et al.
- (ii) TITLE OF INVENTION: Targeted Cytolysis of HIV-Infected Cells by  
Chimeric CD4 Receptor-Bearing Cells
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Fish & Richardson  
(B) STREET: 225 Franklin Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
(B) COMPUTER: IBM PS/2 Model 50Z or 55SX  
(C) OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
(D) SOFTWARE: Wordperfect (Version 5.0)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/847,566  
(B) FILING DATE: March 6, 1992  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/665,961  
(B) FILING DATE: March 7, 1991  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Clark, Paul T.  
(B) REGISTRATION NUMBER: 30,162  
(C) REFERENCE/DOCKET NUMBER: 00786/212001
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (617) 542-5070  
(B) TELEFAX: (617) 542-8906  
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1728 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAACCGGG	GAGTCCCTTT	TAGGCACTTG	CTTCTGGTGC	TGCAACTGGC	50
GCTCCTCCCA	GCAGCCACTC	AGGGAAACAA	AGTGGTGCTG	GGCAAAAAAG	100
GGGATACAGT	GGAAGTGACC	TGTACAGCTT	CCCAGAAGAA	GAGCATACAA	150
TTCCACTGGA	AAAAGTCCAA	CCAGATAAAG	ATTCTGGGAA	ATCAGGGCTC	200
CTTCTTAACT	AAAGGTCCAT	CCAAGCTGAA	TGATCGCGCT	GACTCAAGAA	250
GAAGCCTTTG	GGACCAAGGA	AAGTTCCCCC	TGATCATCAA	GAATCTTAAG	300
ATAGAAGACT	CAGATACTTA	CATCTGTGAA	GTGGAAGACC	AGAAGGAGGA	350
GGTGCAATTG	CTAGTGTTTG	GATTGACTGC	CAACTCTGAC	ACCCACCTGC	400
TTCAGGGGCA	GAGCCTGACC	CTGACCTTGG	AGAGCCCCCC	TGGTAGTAGC	450
CCCTCAGTGC	AATGTAGGAG	TCCAAGGGGT	AAAAACATAC	AGGGGGGGAA	500
GACCCCTCTC	GTGTCTCAGC	TGGAGCTCCA	GGATAGTGGC	ACCTGGACAT	550
GCACTGTCTT	GCAGAACCAG	AAGAAGGTGG	AGTTCAAAAT	AGACATCGTG	600
GTGCTAGCTT	TCCAGAAGGC	CTCCAGCATA	GTCTATAAGA	AAGAGGGGGA	650
ACAGGTGGAG	TTCTCCTTCC	CACTCGCCTT	TACAGTTGAA	AAGCTGACGG	700
GCACTGGCGA	GCTGTGGTGG	CAGGCGGAGA	GGGCTTCCTC	CTCCAAGTCT	750
TGGATCACCT	TTGACCTGAA	GAACAAGGAA	GTGTCTGTAA	AACGGGTTAC	800
CCAGGACCCT	AAGCTCCAGA	TGGGCAAGAA	GCTCCCGCTC	CACCTCACCC	850
TGCCCCAGGC	CTTGCCTCAG	TATGCTGGCT	CTGGAACCTT	CACCCTGGCC	900
CTTGAAGCGA	AAACAGGAAA	GTTGCATCAG	GAAGTGAACC	TGGTGGTGAT	950
GAGAGCCACT	CAGCTCCAGA	AAAATTTGAC	CTGTGAGGTG	TGGGGACCCA	1000
CCTCCCCTAA	GCTGATGCTG	AGCTTGAAC	TGGAGAACAA	GGAGGCAAAG	1050
GTCTCGAAGC	GGGAGAAGCC	GGTGTGGGTG	CTGAACCCTG	AGGCGGGGAT	1100
GTGGCAGTGT	CTGCTGAGTG	ACTCGGGACA	GGTCTGCTG	GAATCCAACA	1150
TCAAGGTTCT	GCCACATGG	TCCACCCCGG	TGCACGCGGA	TCCCAAATCT	1200
TGCTACTTGC	TAGATGGAAT	CCTCTTCATC	TACGGAGTCA	TCATCACAGC	1250
CCTGTACCTG	AGAGCAAAAT	TCAGCAGGAG	TGCAGAGACT	GCTGCCAACC	1300
TGCAGGACCC	CAACCAGCTC	TACAATGAGC	TCAATCTAGG	GCGAAGAGAG	1350
GAATATGAGC	TCTTGGAGAA	GAAGCGGGCT	CGGGATCCAG	AGATGGGAGG	1400
CAAAACAGCAG	AGGAGGAGGA	ACCCCCAGGA	AGGCGTATAC	AATGCACTGC	1450
AGAAAGACAA	GATGCCAGAA	GCCTACAGTG	AGATCGGCAC	AAAAGGCGAG	1500

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AGGCGGAGAG GCAAGGGGCA CGATGGCCTT TACCAGGACA GCCACTTCCA	1550
AGCAGTGCAG TTCGGGAACA GAAGAGAGAG AGAAGGTTCA GAACTCACAA	1600
GGACCCCTGG GTTAAGAGCC CGCCCCAAAG GTGAAAGCAC CCAGCAGAGT	1650
AGCCAATCCT GTGCCAGCGT CTTCAGCATC CCCACTCTGT GGAGTCCATG	1700
GCCACCCAGT AGCAGCTCCC AGCTCTAA	1728

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC	50
GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG	100
GGGATACAGT GGAAGTGACC TGTACAGCTT CCCAGAAGAA GAGCATACAA	150
TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGCTC	200
CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT GACTCAAGAA	250
GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA GAATCTTAAG	300
ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA	350
GGTGCAATTG CTAGTGTTTG GATTGACTGC CAACTCTGAC ACCCACCTGC	400
TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC	450
CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAACATAC AGGGGGGGGA	500
GACCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT	550
GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT AGACATCGTG	600
GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA	650
ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG	700
GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT	750
TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTTAC	800
CCAGGACCTT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTACCCC	850
TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC TGGTGGTGAT	950

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GAGAGCCACT CAGCTCCAGA AAAATTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA GGAGCCAAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTCTGCTG GAATCCAACA	1150
TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA TCCGCAGCTC	1200
TGCTATATCC TGGATGCCAT CCTGTTTTTG TATGGTATTG TCCTTACCCT	1250
GCTCTACTGT CGACTCAAGA TCCAGGTCCG AAAGGCAGAC ATAACCAGCC	1300
GTGAGAAATC AGATGCTGTC TACACGGGCC TGAACACCCG GAACCAGGAG	1350
ACATATGAGA CTCTGAAACA TGAGAAACCA CCCCAATAG	1389

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC	50
GCTCCTCCCA GCAGCCACTC AGGGAACAA AGTGGTGCTG GGCAAAAAAG	100
GGGATACAGT GGAACGACC TGTACAGCTT CCCAGAAGAA GAGCATACAA	150
TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGCTC	200
CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCCGCT GACTCAAGAA	250
GAAGCCTTTG GGACCAAGGA AACTTCCCC TGATCATCAA GAATCTTAAG	300
ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA	350
GGTGCAATTG CTAGTGTTG GATTGACTGC CAACTCTGAC ACCCACCTGC	400
TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC	450
CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC AGGGGGGGAA	500
GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT	550
GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT AGACATCGTG	600
GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA	650
ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG	700
GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT	750

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TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTTAC	800
CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC	850
TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGCAACAG GAAGTGAACC TGGTGGTGAT	950
GAGAGCCACT CAGCTCCAGA AAAATTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCTAA GCTGATGCTG AGCTTGAAC TGGAGAACAA GGAGGCAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCCCTGCTG GAATCCAACA	1150
TCAAGGTTCT GCCCACAATG TCCACCCCGG TGCACGCGGA TCCCAAACCTC	1200
TGCTACCTGC TGGATGGAAT CCTCTTCATC TATGGTGTCA TTCTCACTGC	1250
CTTGTTCTCTG AGAGTGAAGT TCAGCAGGAG CGCAGAGCCC CCCGCGTACC	1300
AGCAGGGCCA GAACCAGCTC TATAACGAGC TCAATCTAGG ACGAAGAGAG	1350
GAGTACGATG TTTTGGACAA GAGACGTGGC CGGACCCTG AGATGGGGGG	1400
AAAGCCGAGA AGGAAGAACC CTCAGGAAGG CCTGTACAAT GAACTGCAGA	1450
AAGATAAGAT GCGGGAGGCC TACAGTGAGA TTGGGATGAA AGGCGAGCGC	1500
CGGAGGGGCA AGGGGCACGA TGGCCTTTAC CAGGGTCTCA GTACAGCCAC	1550
CAAGGACACC TACGACGCCC TTCACATGCA GGCCCTGCCC CCTCGCTAA	1599

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 575 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Leu	Val	Leu	Gln	Leu
1				5					10					15	
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly	Lys
			20					25					30		
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser
		35				40						45			
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn
	50				55				60						
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala
	65			70				75					80		
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile
			85				90						95		
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu
		100			105							110			
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn
	115					120						125			

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(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 462 amino acids

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Leu	Val	Leu	Gln	Leu
1				5					10					15	
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly	Lys
			20					25					30		
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser
		35					40					45			
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn
	50					55					60				
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala
	65				70					75				80	
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile
				85				90						95	
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu
			100					105					110		
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn
		115					120					125			
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu
	130					135						140			
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly
	145				150					155					160
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu
			165					170						175	
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys
			180					185					190		
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser
		195					200					205			
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
	210					215					220				
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp
	225				230						235				240
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu
			245						250					255	
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu
			260					265					270		
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu
		275					280					285			
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys
	290					295					300				
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr
	305				310						315				320
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro
			325						330					335	
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
			340					345					350</		

435 440 445  
Gln Glu Thr Tyr Glu Thr Leu Lys His Glu Lys Pro Pro Gln  
450 455 460 462

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 532 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Leu	Val	Leu	Gln	Leu
1				5					10					15	
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly	Lys
			20					25					30		
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser
		35					40					45			
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn
	50					55					60				
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala
65					70					75				80	
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile
			85						90					95	
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu
			100					105					110		
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn
		115					120					125			
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu
130						135					140				
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly
145					150					155					160
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu
			165						170					175	
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys
			180					185					190		
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser
		195					200						205		
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
	210					215					220				
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp
225					230					235				240	
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu
			245						250					255	
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu
		260						265					270		
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu
	275						280						285		
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys
	290					295						300			
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr
305					310					315					320
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro
			325						330					335	
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
		340						345						350	
Lys	Arg	Glu	Lys	Pro	Val	Trp	Val	Leu	Asn	Pro	Glu	Ala	Gly	Met	Trp
		355					360						365		

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Gln	Cys	Leu	Leu	Ser	Asp	Ser	Gly	Gln	Val	Leu	Leu	Glu	Ser	Asn	Ile
	370					375					380				
Lys	Val	Leu	Pro	Thr	Trp	Ser	Thr	Pro	Val	His	Ala	Asp	Pro	Lys	Leu
385					390					395					400
Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu	Phe	Ile	Tyr	Gly	Val	Ile	Leu	Thr
				405					410					415	
Ala	Leu	Phe	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Glu	Pro	Pro	Ala
			420					425					430		
Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
	435						440					445			
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu
	450					455					460				
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn
465					470					475					480
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met
				485					490					495	
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly
			500					505					510		
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala
		515					520					525			
Leu	Pro	Pro	Arg												
															530

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCGGGGTGA CCGTGCCCTC CAGCAGCTTG GGC

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGGGATC CGTCGTCCAG AGCCCGTCCA GCTCCCCGTC CTGGGCCTCA

50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

101230 455555



- (A) LENGTH: 48 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGGGGAGC TCGTTATAGA GCTGGTTTGC CGCCGAATTC TTATCCCG

48

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGGGCGG CCACGCGTCC TCGCCAGCAC ACA

33

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGGGACGC GTTTCAGCCG TCCTCGCCAG CACACA

36

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGGACGC GTGACCCTGA GATGGGGGGA AAG

33

(2) INFORMATION FOR SEQ ID NO:17:

099999.02401  
104220.455650

(A) LENGTH: 33 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

33

(A) LENGTH: 26 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

26

(A) LENGTH: 42 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

42

(A) LENGTH: 30 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

**30**

(2) INFORMATION FOR SEQ ID NO:21:

32

31

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGTTGGTTT CTTGAGGTTG TGTCTTTCTG A

31

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu  
5 10 15  
Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg  
20 25 30  
Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val  
35 40 45  
Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile  
50 55 60  
Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys  
65 70 75 80  
Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys  
85 90 95  
Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val  
100 105 110  
Ala Ile Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His  
115 120 125  
Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg  
130 135 140  
Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr  
145 150 155 160  
Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu  
5 10 15  
Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His Leu Val Lys  
20 25 30  
Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala  
35 40 45  
Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe  
50 55 60

(2) INFORMATION FOR SEQ ID NO:26:

(A) LENGTH: 220 amino acids

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(2) INFORMATION FOR SEQ ID NO:27:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

[illegible]